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ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/902,432DATE: 04/23/2002 P16
TIME: 15:29:06Input Set : A:\09902432sequencelisting.txt
Output Set: N:\CRF3\04232002\I902432.raw

3 <110> APPLICANT: Irwin H. Gelman
4 Susan G. Jaken
6 <120> TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
9 <130> FILE REFERENCE: A30558-A-FWC-A 070156.0597
11 <140> CURRENT APPLICATION NUMBER: 09/902,432
C--> 12 <141> CURRENT FILING DATE: 2002-04-08
14 <150> PRIOR APPLICATION NUMBER: 08/978,277
15 <151> PRIOR FILING DATE: 1997-11-25
17 <150> PRIOR APPLICATION NUMBER: 08/665,401
18 <151> PRIOR FILING DATE: 1996-06-18
20 <150> PRIOR APPLICATION NUMBER: 08/635,121
21 <151> PRIOR FILING DATE: 1996-04-19
23 <160> NUMBER OF SEQ ID NOS: 35
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 5134
29 <212> TYPE: DNA
30 <213> ORGANISM: Rattus norvegicus
32 <400> SEQUENCE: 1
33 ggaaaagaca gagccagcct cgaggaggca ggagccggca gaagacacag accaggccag 60
34 gttgtcagca gactacgaga agtgtggagct gccttggaa gaccagggtg gtgacctgga 120
35 ggcatcgtca gaggagaagt gtgctcctt ggcaacggaa gtgtttgatg agaagatgga 180
36 agcccaccaa gaagttgttg cagagggtcca cgtgagcacc gtggagaaga cagaggagga 240
37 gcaaggagga ggaggagagg ctgaaggggg cgtgggtta gaaggaacag gagaatcctt 300
38 gccccctgag aaactggctg agccccagga ggtcccccag gaagctgagc ctgctgagga 360
39 gctgatgaag agcagagaga tgtgtgtctc tggaggagac cacactcaac tgacagacct 420
40 aagtccctgaa gagaagacgc tgcccaaaca cccagaaggc attgtcagtg aggtggagat 480
41 gctgtccctc caggaagaa tcaaggtaca gggaaatccc ttgaagaaac ttttcagtag 540
42 ctcaggctta aagaagctgt ctggaaagaa gcagaagggg aaacgaggag gtgggggaga 600
43 cgaagagcct ggagaatacc aacacattca caccgaatcc ccagagagt ctgatgagca 660
44 gaagggagag agctctgcgt cgtcccccga ggacgcctgag gagaccacgt gtctggagaa 720
45 agggccgctg gaagcacccca ggtatggggaa gctgaggaag gaactacttc gtggagagaa 780
46 gaagaggaag gatcactccc tgggcattct tcaaaaagat ggtgacacccc aagaaacgg 840
47 ccgaagacct tctgagagt acaaggagga agagctggag aaggtcaaga gcccacctt 900
48 gtctccact gatagcacag tgtcagaaat gcaagatgaa gtcaaaaactt ttggtgagga 960
49 acaaaaagcca gaggaaccaa agcgttaggtt ggataactca gtgtcttggg aagcactgat 1020
50 ttgtgtcggta tcatccaaga agagagcaag gaaggcatcc ttttcagata taagagggcc 1080
51 aaggacactg ggagggggac agtcacagag cagaggaggc cagcaaagac aaagaagccg 1140
52 aacagacgct gttcctgcctt gcacccagga gcaggaccaa ggcgaaggaa gttcctcacc 1200
53 cgagccagcg ggaagccctt ccgaagggga aggtgtctcc acttggggagt catttaaaag 1260
54 attagtcaact ccaagaaaaa aatccaagtc aaaactggaa gagaagaag ccggaaaggac 1320
55 tctagttgta ggagcaggtt gttccactgag atcgaaccgt gtagagaaga atcttgggtt 1380
56 tccattaaga aattcatccc cgacggcgg aagaaaaggc cagatggaa ggcaagaaca 1440

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57 agccactgtg gaagactca gggcagtgg aataatgag gacgagctg atgtcccagc 1500
58 cgtcgtgcct ctgtctgag atgatgcgt ggagagggag aagatggaa cccaggggaa 1560
59 tgccggactg cccagctgt ggggctgtgt agtgcgtc gagctcagta agactctgtt 1620
60 ccacactgtg agtgcgtcag tcattgtgg gaccaggca gtcaccagt tcgaagagcg 1680
61 gtccttcctg tggatatccg cttccgtaa agaacctttaa gaacacacag cgggagaagc 1740
62 catgccacct gttgaagagg tcactgaaaa agacatcatt gcagaagaaa ctccgtgtct 1800
63 caccaggacg ttaccaggag gtaaagatgc ccatgacgac atggtcacca gtgaagtgga 1860
64 tttcacctca gaagctgtga cagccacaga gacccagag gtcctccgtta ctgaagaagt 1920
65 taccgaagca tcggggcccg aagagaccac agacatgggt tccgcagttt cccagctgac 1980
66 tgactccccca gacaccacag aggaagccac cccagttcag gaggttagagg gtgggtgtct 2040
67 agatacagaa gaagaggagc gccagacgca ggcattcctc caagccgtt cagacaaggt 2100
68 gaaagaggag tcccgaggc tcgcaaccca gactgtgcag agaacgggtt caaaaggact 2160
69 ggagaagggtt gaggagtag aggaggactc cgaagtgcgt gttcggaga aagagaagga 2220
70 cgttatgcccg aaaggaccccg tgccaggaaagc tggagctgag catcttgcac agggctctga 2280
71 gactggacag gctactccag agagccttga agttctgaa gtcacagcag atgttagacca 2340
72 tgcgccacg tgccaggtt tcaagctcca gcagctgatg gaacaggccg tggccctgt 2400
73 gtcatccgaa accttgacag acagtggagac aaatggaagc actcccttag cagattcaga 2460
74 cactgcagat gggacacagc aagatgaaac cattgacagc caggacagta aagccactgc 2520
75 agctgtcagg cagtcacagg tcacagaaga agaggcggct actgctcaga aagaggagcc 2580
76 ttcgacacta cctaataatg ttccagccca ggaagaacat ggggaagaac caggaagaga 2640
77 tttcttgaa cctacacagc aagagcttgc tgctgcagcc gtgcccgtct ggcaaaagac 2700
78 tgaggtgggt caagagggtg agttgactg gttggatgg aaaaaagtca aagaagaaca 2760
79 ggaggtgttt gtacactctg gacccaacag tcaaaaaggct gctgtatgtca catatgacag 2820
80 tgaagtgtat ggagtggccg ggtgtcagga aaaggagagt actgaagtgc agagtcttag 2880
81 cctggaggag ggagagatgg aaactgacgt tgaaaaaggag aaaagggaga caaagccaga 2940
82 gcaagtgtatg gaagaagggtg agcaggaaac agccgtctt gaggatgaaa ggaactacgg 3000
83 gaagccagtc ctgacactt acatgcccac ctcagagagg gggaggcac tggaaagcc 3060
84 tggaggaagc cttctctcc cagaccaaga caaagcagggt tgcatagagg ttcaagttca 3120
85 aagctggac acaacagtca ctcacacagc agaagctgtg gaaaagggtca tagaaacgg 3180
86 tttgtattca gagacagggtg aaagtccaga gtgtgttaggt gcacacttat taccagctga 3240
87 gaagtcctct gcaacgggtg gccactggac tttcagcat gcagaggaca cggtaccct 3300
88 ggggccttag ttcagggcag aatccatccc aatcatgtt actctctgtc ctgaaagcc 3360
89 cctacatctt gacccataag gagaataaaag cgcacccag agagagcgt cagaggaaga 3420
90 ggacaaggcca gatgtggtc ctgtatgtca cggcaaggag agtacagcaa tcgacaaagt 3480
91 cctcaaggctt gaaacctgaga tcctggaaact tgagagtaag agcaacaaga ttgtgtgt 3540
92 cgtcattcag acagccgtt accagttcgc acgtacagaa acagccccccg aaactcatgc 3600
93 ttatgattca cagacccagg ttccgtcaat ggcgttggac agcaggggagc ccaacagatg 3660
94 ctggacaaaa atgaaagttt ccaagatgaa acacccagtg cccgagccca gagaggactt 3720
95 gcaagtctgtt accgttctgg aggcattggc cagctggaa atgttgcgt cgctgtcagt 3780
96 tggaaagcgcc ggtgtcaaag taagcattga gaagctgtt cctcaacccca aagatcaaaa 3840
97 ggagcatgtt gctgtatggcc ctcagatcca aagcttagcc caggcagagg cagtgtctgg 3900
98 aaacctaacc aaagaatccc cagacacccaa cggaccaaaag ctaaccgggg agcgtatgccc 3960
99 ccaaaaagttt aggtccagga agaagaaaatg tctaccaagt cagtcaaaga gaacaaggcc 4020
100 caggcagaag aggacctca ggagccaaag ggagacctgg cagaatccta agatgttagt 4080
101 tgctcattgtt acatctgtt gaccggatg tgaaaacaag tcacagaaca agatgtctgt 4140
102 gttgggaccc tggaccaaga tttcagggcc catgagatcc agagagcagg gccgtccaaat 4200
103 gattccacc cagtagagca ccccgacaaat tctgaggctt catcggggagc tagagccagc 4260
104 taacatttcc tcgttcaag actgcctttt atttccccct tcatqccqtc cqtqatttc 4320
105 taacatttcc tcgttcaag actgcctttt atttccccct tcatqccqtc cqtqatttc 4380

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106 ggatttaagg tcctgcgttc tcaacctgga accaattctg ccataccctag ttccacttct 4440
 107 caaactggag catccctcctt tatgtattta tatgtatgtt ttatgtatgc ctccctctgt 4500
 108 acctattgtta tatttttttc taacgtttaa gcacatgctt tttgtattat gcaatatata 4560
 109 acgggtgtgc agccatagcg acgctttgaa aagctccaag cctcaactgt aacctgcagc 4620
 110 aaacagataa cattcctggc aagaagagac aagtctttt taaagttac tgatgcttag 4680
 111 atctgtgggc ttcttagtcct ctgaaaatgg ttgtttccct atgcacagcg agctcagaaa 4740
 112 taaaaacccc atttgaaac atccaggatg tcccaatatt accatgattt tttcccccct 4800
 113 ttttgctaat ccagtccagg ttggaaaagaa gtctccctgt tgtcagatta agccctgtct 4860
 114 cttaatgata tggacaaatg agtgtgccta aggccatgag atgtttccta atgcagaagg 4920
 115 aatctgtgt acgtttttt gattgtactc ttctatgctg gaccgaattc atatgcagat 4980
 116 cgaagtgagt cctgttctt acagatggta ttttgataga tactggagtt tgctgtgtt 5040
 117 atatctgtgc cccttcttta agaacaatgt tgcattatgt tcctttggat aaattgtgat 5100
 118 ttgacaactg atttaaataa acatatttga ctac 5134
 122 <210> SEQ ID NO: 2
 123 <211> LENGTH: 1346
 124 <212> TYPE: PRT
 125 <213> ORGANISM: Rattus norvegicus
 127 <400> SEQUENCE: 2
 128 Met Glu Ala His Gln Glu Val Val Ala Glu Val His Val Ser Thr Val
 129 1 5 10 15
 130 Glu Lys Thr Glu Glu Glu Gln Gly Gly Gly Glu Ala Glu Gly Gly
 131 20 25 30
 132 Val Val Val Glu Gly Thr Gly Glu Ser Leu Pro Pro Glu Lys Leu Ala
 133 35 40 45
 134 Glu Pro Gln Glu Val Pro Gln Glu Ala Glu Pro Ala Glu Glu Leu Met
 135 50 55 60
 136 Lys Ser Arg Glu Met Cys Val Ser Gly Gly Asp His Thr Gln Leu Thr
 137 65 70 75 80
 138 Asp Leu Ser Pro Glu Glu Lys Thr Leu Pro Lys His Pro Glu Gly Ile
 139 85 90 95
 140 Val Ser Glu Val Glu Met Leu Ser Ser Gln Glu Arg Ile Lys Val Gln
 141 100 105 110
 142 Gly Ser Pro Leu Lys Lys Leu Phe Ser Ser Ser Gly Leu Lys Lys Leu
 143 115 120 125
 144 Ser Gly Lys Lys Gln Lys Gly Lys Arg Gly Gly Gly Asp Glu Glu
 145 130 135 140
 146 Pro Gly Glu Tyr Gln His Ile His Thr Glu Ser Pro Glu Ser Ala Asp
 147 145 150 155 160
 148 Glu Gln Lys Gly Glu Ser Ser Ala Ser Ser Pro Glu Glu Pro Glu Glu
 149 165 170 175
 150 Thr Thr Cys Leu Glu Lys Gly Pro Leu Glu Ala Pro Arg Met Gly Lys
 151 180 185 190
 152 Leu Arg Lys Glu Leu Leu Arg Gly Glu Lys Lys Arg Lys Asp His Ser
 153 195 200 205
 154 Leu Gly Ile Leu Gln Lys Asp Gly Asp Thr Gln Glu Thr Val Arg Arg
 155 210 215 220
 156 Pro Ser Glu Ser Asp Lys Glu Glu Glu Leu Glu Lys Val Lys Ser Ala
 157 225 230 235 240
 158 Thr Leu Ser Ser Thr Asp Ser Thr Val Ser Glu Met Gln Asp Glu Val

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| | | | |
|-----|---|-----|-----|
| 159 | 245 | 250 | 255 |
| 160 | Lys Thr Val Gly Glu Glu Gln Lys Pro Glu Glu Pro Lys Arg Arg Val | | |
| 161 | 260 | 265 | 270 |
| 162 | Asp Thr Ser Val Ser Trp Glu Ala Leu Ile Cys Val Gly Ser Ser Lys | | |
| 163 | 275 | 280 | 285 |
| 164 | Lys Arg Ala Arg Lys Ala Ser Ser Ser Asp Ile Arg Gly Pro Arg Thr | | |
| 165 | 290 | 295 | 300 |
| 166 | Leu Gly Gly Gln Ser Gln Ser Arg Gly Gly Gln Gln Arg Gln Arg | | |
| 167 | 305 | 310 | 315 |
| 168 | Ser Arg Thr Asp Ala Val Pro Ala Ser Thr Gln Glu Gln Asp Gln Ala | | |
| 169 | 325 | 330 | 335 |
| 170 | Gln Gly Ser Ser Ser Pro Glu Pro Ala Gly Ser Pro Ser Glu Gly Glu | | |
| 171 | 340 | 345 | 350 |
| 172 | Gly Val Ser Thr Trp Glu Ser Phe Lys Arg Leu Val Thr Pro Arg Lys | | |
| 173 | 355 | 360 | 365 |
| 174 | Lys Ser Lys Ser Lys Leu Glu Glu Lys Glu Ala Gly Arg Thr Leu Val | | |
| 175 | 370 | 375 | 380 |
| 176 | Val Gly Ala Gly Cys Pro Leu Arg Ser Asn Arg Val Glu Lys Asn Leu | | |
| 177 | 385 | 390 | 395 |
| 178 | Gly Phe Pro Leu Arg Asn Ser Ser Pro Asp Gly Gly Arg Lys Gly Gln | | |
| 179 | 405 | 410 | 415 |
| 180 | Met Gly Arg Gln Glu Gln Ala Thr Val Glu Asp Ser Gly Pro Val Glu | | |
| 181 | 420 | 425 | 430 |
| 182 | Ile Asn Glu Asp Glu Pro Asp Val Pro Ala Val Val Pro Leu Ser Glu | | |
| 183 | 435 | 440 | 445 |
| 184 | Tyr Asp Ala Val Glu Arg Glu Lys Met Glu Ala Gln Gly Asn Ala Glu | | |
| 185 | 450 | 455 | 460 |
| 186 | Leu Pro Ser Cys Trp Gly Cys Val Val Ser Glu Glu Leu Ser Lys Thr | | |
| 187 | 465 | 470 | 475 |
| 188 | 480 | | |
| 189 | Leu Val His Thr Val Ser Val Ala Val Ile Asp Gly Thr Arg Ala Val | | |
| 190 | 485 | 490 | 495 |
| 191 | Thr Ser Val Glu Glu Arg Ser Pro Ser Trp Ile Ser Ala Ser Val Thr | | |
| 192 | 500 | 505 | 510 |
| 193 | 515 | 520 | 525 |
| 194 | Glu Pro Leu Glu His Thr Ala Gly Glu Ala Met Pro Pro Val Glu Glu | | |
| 195 | 530 | 535 | 540 |
| 196 | Val Thr Glu Lys Asp Ile Ile Ala Glu Glu Thr Pro Val Leu Thr Gln | | |
| 197 | 545 | 550 | 555 |
| 198 | 560 | | |
| 199 | Thr Leu Pro Glu Gly Lys Asp Ala His Asp Asp Met Val Thr Ser Glu | | |
| 200 | 565 | 570 | 575 |
| 201 | Val Asp Phe Thr Ser Glu Ala Val Thr Ala Thr Glu Thr Ser Glu Ala | | |
| 202 | 580 | 585 | 590 |
| 203 | Leu Arg Thr Glu Glu Val Thr Glu Ala Ser Gly Ala Glu Glu Thr Thr | | |
| 204 | 595 | 600 | 605 |
| 205 | Asp Met Val Ser Ala Val Ser Gln Leu Thr Asp Ser Pro Asp Thr Thr | | |
| 206 | 610 | 615 | 620 |
| 207 | Glu Glu Glu Glu Arg Gln Thr Gln Ala Ile Leu Gln Ala Val Ala Asp | | |
| | 625 | 630 | 635 |
| | | | 640 |

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208 Lys Val Lys Glu Glu Ser Gln Val Pro Ala Thr Gln Thr Val Gln Arg
209 645 650 655
210 Thr Gly Ser Lys Ala Leu Glu Lys Val Glu Glu Val Glu Glu Asp Ser
211 660 665 670
212 Glu Val Leu Ala Ser Glu Lys Glu Lys Asp Val Met Pro Lys Gly Pro
213 675 680 685
214 Val Gln Glu Ala Gly Ala Glu His Leu Ala Gln Gly Ser Glu Thr Gly
215 690 695 700
216 Gln Ala Thr Pro Glu Ser Leu Glu Val Pro Glu Val Thr Ala Asp Val
217 705 710 715 720
218 Asp His Val Ala Thr Cys Gln Val Ile Lys Leu Gln Gln Leu Met Glu
219 725 730 735
220 Gln Ala Val Ala Pro Glu Ser Ser Glu Thr Leu Thr Asp Ser Glu Thr
221 740 745 750
222 Asn Gly Ser Thr Pro Leu Ala Asp Ser Asp Thr Ala Asp Gly Thr Gln
223 755 760 765
224 Gln Asp Glu Thr Ile Asp Ser Gln Asp Ser Lys Ala Thr Ala Ala Val
225 770 775 780
226 Arg Gln Ser Gln Val Thr Glu Glu Ala Ala Thr Ala Gln Lys Glu
227 785 790 795 800
228 Glu Pro Ser Thr Leu Pro Asn Asn Val Pro Ala Gln Glu Glu His Gly
229 805 810 815
230 Glu Glu Pro Gly Arg Asp Val Leu Glu Pro Thr Gln Gln Glu Leu Ala
231 820 825 830
232 Ala Ala Ala Val Pro Val Trp Gln Lys Thr Glu Val Gly Gln Glu Gly
233 835 840 845
234 Glu Val Asp Trp Leu Asp Gly Glu Lys Val Lys Glu Glu Gln Glu Val
235 850 855 860
236 Phe Val His Ser Gly Pro Asn Ser Gln Lys Ala Ala Asp Val Thr Tyr
237 865 870 875 880
238 Asp Ser Glu Val Met Gly Val Ala Gly Cys Gln Glu Lys Glu Ser Thr
239 885 890 895
240 Glu Val Gln Ser Leu Ser Leu Glu Glu Gly Glu Met Glu Thr Asp Val
241 900 905 910
242 Glu Lys Glu Lys Arg Glu Thr Lys Pro Glu Gln Val Ser Glu Glu Gly
243 915 920 925
244 Glu Gln Glu Thr Ala Ala Pro Glu His Glu Arg Asn Tyr Gly Lys Pro
245 930 935 940
246 Val Leu Thr Leu Asp Met Pro Ser Ser Glu Arg Gly Lys Ala Leu Gly
247 945 950 955 960
248 Ser Leu Gly Gly Ser Pro Ser Leu Pro Asp Gln Asp Lys Ala Gly Cys
249 965 970 975
250 Ile Glu Val Gln Val Gln Ser Leu Asp Thr Thr Val Thr Gln Thr Ala
251 980 985 990
252 Glu Ala Val Glu Lys Val Ile Glu Thr Val Val Ile Ser Glu Thr Gly
253 995 1000 1005
254 Glu Ser Pro Glu Cys Val Gly Ala His Leu Leu Pro Ala Glu Lys Ser
255 1010 1015 1020
256 Ser Ala Thr Gly His Trp Thr Leu Gln His Ala Glu Asp Thr Val

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/23/2002
PATENT APPLICATION: US/09/902,432 TIME: 15:29:07

Input Set : A:\09902432sequencelisting.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:19; Xaa Pos. 3,4,5,7,11,12,16,18,19,20

Seq#: 21; Xaa Pos. 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38

Seq#:21; Xaa Pos. 39,40,41,42,43,44,45,46

Seq#: 22; Xaa Pos. 6, 7, 8, 9

VERIFICATION SUMMARY

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Input Set : A:\09902432sequencelisting.txt

Output Set: N:\CRF3\04232002\I902432.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:812 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:816 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:820 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:824 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:828 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:832 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:836 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:840 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:844 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:848 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:849 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:851 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:16
L:881 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:16
L:883 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:32
L:900 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:1049 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1053 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:35
L:1057 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:35